## JAN 2 9 2002 ...

## SEQUENCE LISTING

<110> Hauptmannaput 1ph
 Himmler, Adolph
 Maurer-Fogy, Ingrid
 Stratowa, Christian

<120> TNF Receptors, TNF Binding Proteins and DNAs Coding for Them

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<150> 09/525,998 <151> 2000-03-15

<150> 08/383,676 <151> 1995-02-01

<150> 08/153,287 <151> 1993-11-17

<150> 07/821,750 <151> 1992-01-02

<150> 07/511,430 . <151> 1990-04-20

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TECH CENTER 1600/2900

## extracellular proteases following secretion

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gag atc t Glu Ile S											384
aag aac c Lys Asn G 130											432
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		Thr		ttc Phe							864
	_			tcc Ser 295	_						912
				cgc Arg							960
				aca Thr							1008
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				ctg Leu							1104
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35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys 50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp 65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val 100 105 110

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys 225 230 235 240

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agt gaa aac o Ser Glu Asn I 1	_	_	n Cys Ser Leu	-	
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Phe Thr Ala S	Ser Glu Asn	His Leu Arg	g His Cys Leu 60	_	Lys

65 70 75 80	
Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp 85 90 95	
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Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys 115 120 125	
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Cys His Ala (	Gly Phe Phe	Leu Arg Gl	u Asn Glu Cys 140	Val Ser Cys	Ser
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			a ggc ccg ggg o Gly Pro Gly 75		
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Lys Gln Asn	Thr Val	-	Cys		ala Gly .70	Phe	Phe	Leu	Arg 175	Glu	
Asn Glu Cys	Val Ser 180	Cys Ser		Cys L 185	ys Lys	Ser	Leu	Glu 190	Cys	Thr	
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85	90	95
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Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe 130 135 140	
Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser 145 150 155 160	
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Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro	92
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Arg H				agc Ser												336
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Lys Gln Asn	Thr Val 165	Cys Thr	Cys His	Ala Gly 170	Phe Phe	Leu Ar 17		
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Met Gly Gln	gtg gag Val Glu 85											288
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Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe 130 135 140	
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acc aag tgc cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg 1997.  Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro  50 55 60	2
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tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc aaa tgc cga aag 28. Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys 85 90 95	8
gaa atg ggt cag gtg gag atc tct tct tgc aca gtg gac cgg gac acc Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr 100 105 110	6
gtg tgt ggc tgc agg aag aac cag tac cgg cat tat tgg agt gaa aac 38. Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn 115 120 125	4

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			c tgc cat gca gg r Cys His Ala Gl 16	У
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Ser Glu Asn His	Leu Arg His Cy 85	s Leu Ser Cys Se 90	r Lys Cys Arg Ly 95	s
Glu Met Gly Gln		er Ser Cys Thr Va 105	l Asp Arg Asp Th	r
Val Cys Gly Cys	Arg Lys Asn Gl		r Trp Ser Glu As 125	n .
Leu Phe Gln Cys	Phe Asn Cys Se	er Leu Cys Leu As 14	n Gly Thr Val Hi O	S
Leu Ser Cys Gln 145	Glu Lys Gln As 150	n Thr Val Cys Th	r Cys His Ala Gl 16	

Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser Asn Cys Lys 170

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48

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tgg agt gaa aac ctt ttc cag tgc ttc aat tgc agc ctc tgc ctc aat 336 Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn 100 105

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aac tgt aag aaa agc ctg gag tgc acg aag ttg tgc cta ccc cag att Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile 145 150 155 gag aat gtt aag ggc act gag gac tca ggc acc aca Glu Asn Val Lys Gly Thr Glu Asp Ser Gly Thr Thr 165 <210> 20 <211> 172 <212> PRT <213> Artificial Sequence <220> <223> Description of Artificial Sequence: recombinant TNF-BP sequence Met Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly 35 Ser Phe Thr Ala Ser Glu Asn His Leu Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu Lys Gln Asn Thr Val Cys Thr 115 120 125 Cys His Ala Gly Phe Phe Leu Arg Glu Asn Glu Cys Val Ser Cys Ser 135 Asn Cys Lys Lys Ser Leu Glu Cys Thr Lys Leu Cys Leu Pro Gln Ile 155

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165

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		_		ctc ttc att Leu Phe Ile 230	
_	_		_	tac tcc att Tyr Ser Ile 245	
				gaa gga act Glu Gly Thr 260	
				act cca ggc Thr Pro Gly	
				acc ttc acc Thr Phe Thr	
				gcg gct ccc Ala Ala Pro 310	
				atc ctt gcg Ile Leu Ala 325	
				aag tgg gag Lys Trp Glu 340	
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His	Leu	Gly 35	Asp	Arg	Glu	Lys	Arg 40	Asp	Ser	Val	Cys	Pro 45	Gln	Gly	Lys
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Cys	Arg	Glu	Cys	Glu 85	Ser	Gly	Ser	Phe	Thr 90	Ala	Ser	Glu	Asn	His 95	Leu
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Glu	Ile	Ser 115	Ser	Cys	Thr	Val	Asp 120	Arg	Asp	Thr	Val	Cys 125	Gly	Cys	Arg
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Pro Asn Phe Ala Ala Pro Arg Glu Val Ala Pro Pro Tyr Gln Gly
                    310
                                        315
Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn
                325
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<210> 24
<211> 2173
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: raTNF-R8

<220>
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<222> (245)..(1627)
<400> 24
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ttgccaattg ctgccctgtc cccagcccca atgggggagt gagagaggcc actgccggcc 240
ggac atg ggt ctc ccc atc gtg cct ggc ctg ctg ctg tca ctg gtg ctc 289  Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu  1 5 10 15
ctg gct ctg ctg atg ggg ata cac cca tca ggg gtc acc gga ctg gtt 337 Leu Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val 20 25 30
cct tct ctt ggt gac cgg gag aag agg gat aat ttg tgt ccc cag gga 385 Pro Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly 35 40 45
aag tat gcc cat cca aag aat aat tcc atc tgc tgc acc aag tgc cac 433 Lys Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His 50 55 60
aaa gga acc tac ttg gtg agt gac tgt cca agc cca ggg cag gaa aca 481 Lys Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr 65 70 75
gtc tgc gag ctc tct cat aaa ggc acc ttt aca gct tcg cag aac cac 529 Val Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His 80 85 90 95
gtc aga cag tgt ctc agt tgc aag aca tgt cgg aaa gaa atg ttc cag 577 Val Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln 100 105 110
gtg gag att tct cct tgc aaa gct gac atg gac acc gtg tgt ggc tgc 625 Val Glu Ile Ser Pro Cys Lys Ala Asp Met Asp Thr Val Cys Gly Cys 115 120 125
aag aag aac caa ttc cag cgc tac ctg agt gag acg cat ttc cag tgt 673 Lys Lys Asn Gln Phe Gln Arg Tyr Leu Ser Glu Thr His Phe Gln Cys 130 135 140
gtg gac tgc agc ccc tgc ttc aat ggc acc gtg aca atc ccc tgt aag 721 Val Asp Cys Ser Pro Cys Phe Asn Gly Thr Val Thr Ile Pro Cys Lys 145 150 155
gag aaa cag aac acc gtg tgt aac tgc cac gca gga ttc ttt cta agc 769 Glu Lys Gln Asn Thr Val Cys Asn Cys His Ala Gly Phe Phe Leu Ser 160 165 170 175
gga aat gag tgc acc cct tgc agc cac tgc aag aaa aat cag gaa tgt 817 Gly Asn Glu Cys Thr Pro Cys Ser His Cys Lys Lys Asn Gln Glu Cys 180 185 190
atg aag ctg tgc cta cct cca gtt gca aat gtc aca aac ccc cag gac  Met Lys Leu Cys Leu Pro Pro Val Ala Asn Val Thr Asn Pro Gln Asp  195 200 205

tca gg													913
ctt tta Leu Lei 22!	ı Phe												961
agg cco Arg Pro 240													1009
gag gte Glu Va													1057
atc cc	_		-										1105
agc acc Ser Th													1153
ccc gte Pro Val 30	l Phe			_							_	-	1201
gag gte Glu Va 320													1249
aac cc Asn Pr													1297
gcg gc													1345
gct gte Ala Va		_			_		_		_		_		1393
ctc ctc Leu Le 38	ı Gly												1441
ggg cg Gly Ar 400													1489
cgc cg Arg Ar		_	_		 _	_	_	_	_	 	_		1537

ctt	tgc	gac	atg	aac	ctg	cgt	ggc	tgc	ctg	gag	aac	atc	cgc	gag	act	1585
Leu	Cys	Asp	Met	Asn	Leu	Arg	Gly	Cys	Leu	Glu	Asn	Ile	Arg	Glu	Thr	
			435					440					445			

cta gaa agc cct gcc cac tcg tcc acg acc cac ctc ccg cga
Leu Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg
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455
460

<210> 25

<211> 461

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: raTNF-R8

<400> 25

Met Gly Leu Pro Ile Val Pro Gly Leu Leu Leu Ser Leu Val Leu Leu
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Ala Leu Leu Met Gly Ile His Pro Ser Gly Val Thr Gly Leu Val Pro 20 25 30

Ser Leu Gly Asp Arg Glu Lys Arg Asp Asn Leu Cys Pro Gln Gly Lys 35 40 45

Tyr Ala His Pro Lys Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Val Ser Asp Cys Pro Ser Pro Gly Gln Glu Thr Val 65 70 75 80

Cys Glu Leu Ser His Lys Gly Thr Phe Thr Ala Ser Gln Asn His Val 85 90 95

Arg Gln Cys Leu Ser Cys Lys Thr Cys Arg Lys Glu Met Phe Gln Val

			100					105					110		
Glu	Ile	Ser 115	Pro	Cys	Lys	Ala	Asp 120	Met	Asp	Thr	Val	Cys 125	Gly	Cys	Lys
Lys	Asn 130	Gln	Phe	Gln	Arg	Tyr 135	Leu	Ser	Glu	Thr	His 140	Phe	Gln	Cys	Val
Asp 145	Cys	Ser	Pro	Cys	Phe 150	Asn	Gly	Thr	Val	Thr 155	Ile	Pro	Cys	Lys	Glu 160
Lys	Gln	Asn	Thr	Val 165	Cys	Asn	Cys	His	Ala 170	Gly	Phe	Phe	Leu	Ser 175	Gly
Asn	Glu	Cys	Thr 180	Pro	Сув	Ser	His	Cys 185	Lys	Lys	Asn	Gln	Glu 190	Cys	Met
Lys	Leu	Cys 195	Leu	Pro	Pro	Val	Ala 200	Asn	Val	Thr	Asn	Pro 205	Gln	Asp	Ser
Gly	Thr 210	Ala	Val	Leu	Leu	Pro 215	Leu	Val	Ile	Phe	Leu 220	Gly	Leu	Cys	Leu
Leu 225	Phe	Phe	Ile	Cys	Ile 230	Ser	Leu	Leu	Cys	Arg 235	Tyr	Pro	Gln	Trp	Arg 240
Pro	Arg	Val	Tyr	Ser 245	Ile	Ile	Cys	Arg	Asp 250	Ser	Ala	Pro	Val	Lys 255	Glu
Val	Glu	Gly	Glu 260	Gly	Ile	Val	Thr	Lys 265	Pro	Leu	Thr	Pro	Ala 270	Ser	Ile
Pro	Ala	Phe 275	Ser	Pro	Asn	Pro	Gly 280	Phe	Asn	Pro	Thr	Leu 285	Gly	Phe	Ser
Thr	Thr 290	Pro	Arg	Phe	Ser	His 295	Pro	Val	Ser	Ser	Thr 300	Pro	Ile	Ser	Pro
Val 305	Phe	Gly	Pro		Asn 310	_	His	Asn		Val 315		Pro	Val		Glu 320
Val	Val	Pro	Thr	Gln 325	Gly	Ala	Asp	Pro	Leu 330	Leu	Tyr	Gly	Ser	Leu 335	Asn
Pro	Val	Pro	Ile 340	Pro	Ala	Pro	Val	Arg 345	Lys	Trp	Glu	Asp	Val 350	Val	Ala
Ala	Gln	Pro 355	Gln	Arg	Leu	Asp	Thr 360	Ala	Asp	Pro	Ala	Met 365	Leu	Tyr	Ala
Val	Val 370	Asp	Gly	Val	Pro	Pro 375	Thr	Arg	Trp	Lys	Glu 380	Phe	Met	Arg	Leu
Leu 385	Gly	Leu	Ser	Glu	His 390	Glu	Ile	Glu	Arg	Leu 395	Glu	Leu	Gln	Asn	Gly 400
Arg	Cys	Leu	Arg	Glu	Ala	His	Tyr	Ser	Met	Leu	Glu	Ala	Trp	Arg	Arg

420 425 430
Cys Asp Met Asn Leu Arg Gly Cys Leu Glu Asn Ile Arg Glu Thr Leu 435 440 445
Glu Ser Pro Ala His Ser Ser Thr Thr His Leu Pro Arg 450 455 460
<210> 26 <211> 2141 <212> DNA <213> Artificial Sequence
<220> <223> Description of Artificial Sequence: human TNF-R in lTNF-R2
<220> <221> CDS <222> (213)(1577)
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ctggacagac cgagtcccgg gaagccccag cactgccgct gccacactgc cctgagccca 180
katgggggag tgagaggcca tagctgtctg gc atg ggc ctc tcc acc gtg cct 233 Met Gly Leu Ser Thr Val Pro 1 5
gac ctg ctg ctg cca ctg gtg ctc ctg gag ctg ttg gtg gga ata tac 281 Asp Leu Leu Pro Leu Val Leu Leu Glu Leu Leu Val Gly Ile Tyr 10 15 20
ccc tca ggg gtt att gga ctg gtc cct cac cta ggg gac agg gag aag 329 Pro Ser Gly Val Ile Gly Leu Val Pro His Leu Gly Asp Arg Glu Lys 25 30 35
aga gat agt gtg tgt ccc caa gga aaa tat atc cac cct caa aat aat 377 Arg Asp Ser Val Cys Pro Gln Gly Lys Tyr Ile His Pro Gln Asn Asn 40 45 50 55
tcg att tgc tgt acc aag tgc cac aaa gga acc tac ttg tac aat gac 425 Ser Ile Cys Cys Thr Lys Cys His Lys Gly Thr Tyr Leu Tyr Asn Asp 60 65 70
tgt cca ggc ccg ggg cag gat acg gac tgc agg gag tgt gag agc ggc 473 Cys Pro Gly Pro Gly Gln Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly 75 80 85
tcc ttc acc gct tca gaa aac cac ctc aga cac tgc ctc agc tgc tcc 521

Arg Thr Pro Arg His Glu Ala Thr Leu Asp Val Val Gly Arg Val Leu

Ser	Phe	Thr 90	Ala	Ser	Glu	Asn	His 95	Leu	Arg	His	Cys	Leu 100	Ser	Cys	Ser	
						ggt Gly 110										569
						ggc Gly										617
						cag Gln										665
						tgc Cys	_			_				_		713
						cta Leu										761
						gag Glu 190										809
		_	_			gag Glu	_									857
_	_					ctt Leu	_									905
	_		_			cgg Arg		_		_					_	953
						gaa Glu										1001
	_		_	_		aac Asn 270		_		_						1049
						agt Ser										1097
						ggt Gly										1145
						tat Tyr										1193

315		320		325	
gcc ctc gcc tcc Ala Leu Ala Ser 330				Trp Glu	
agc gcc cac aag Ser Ala His Lys 345					
tac gcc gtg gtg Tyr Ala Val Val 360					
cgg cgc cta ggg Arg Arg Leu Gly					
aac ggg cgc tgc Asn Gly Arg Cys 395					
agg cgg cgc acg Arg Arg Arg Thr 410				Leu Gly	
gtg ctc cgc gac Val Leu Arg Asp 425					
gcg ctt tgc ggc Ala Leu Cys Gly 440					
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<210> 27 <211> 455 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: human TNF-R in lTNF-R2

<400> 27

Met Gly Leu Ser Thr Val Pro Asp Leu Leu Leu Pro Leu Val Leu Leu
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Glu Leu Leu Val Gly Ile Tyr Pro Ser Gly Val Ile Gly Leu Val Pro 20 25 30

His Leu Gly Asp Arg Glu Lys Arg Asp Ser Val Cys Pro Gln Gly Lys
35 40 45

Tyr Ile His Pro Gln Asn Asn Ser Ile Cys Cys Thr Lys Cys His Lys
50 55 60

Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln Asp Thr Asp
65 70 75 80

Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu Asn His Leu 85 90 95

Arg His Cys Leu Ser Cys Ser Lys Cys Arg Lys Glu Met Gly Gln Val

Glu Ile Ser Ser Cys Thr Val Asp Arg Asp Thr Val Cys Gly Cys Arg 115 120 125

Lys Asn Gln Tyr Arg His Tyr Trp Ser Glu Asn Leu Phe Gln Cys Phe 130 135 140

Asn Cys Ser Leu Cys Leu Asn Gly Thr Val His Leu Ser Cys Gln Glu 145 150 155 160

Lys Gln Asn Thr Val Cys Thr Cys His Ala Gly Phe Phe Leu Arg Glu 165 170 175

Asn Glu Cys Val Ser Cys Ser Asn Cys Lys Lys Ser Leu Glu Cys Thr 180 185 190

Lys Leu Cys Leu Pro Gln Ile Glu Asn Val Lys Gly Thr Glu Asp Ser 195 200 205

Gly Thr Thr Val Leu Leu Pro Leu Val Ile Phe Phe Gly Leu Cys Leu 210 215 220

Leu Ser Leu Leu Phe Ile Gly Leu Met Tyr Arg Tyr Gln Arg Trp Lys 225 230 235 240

Ser Lys Leu Tyr Ser Ile Val Cys Gly Lys Ser Thr Pro Glu Lys Glu 245 250 255

Gly Glu Leu Glu Gly Thr Thr Thr Lys Pro Leu Ala Pro Asn Pro Ser

260 265 270

Phe Ser Pro Thr Pro Gly Phe Thr Pro Thr Leu Gly Phe Ser Pro Val 275 280 285

Pro Ser Ser Thr Phe Thr Ser Ser Ser Thr Tyr Thr Pro Gly Asp Cys 290 295 300

Pro Asn Phe Ala Ala Pro Arg Arg Glu Val Ala Pro Pro Tyr Gln Gly 305 310 315

Ala Asp Pro Ile Leu Ala Thr Ala Leu Ala Ser Asp Pro Ile Pro Asn 325 330 335

Pro Leu Gln Lys Trp Glu Asp Ser Ala His Lys Pro Gln Ser Leu Asp 340 345 350

Thr Asp Asp Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro 355 360 365

Leu Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu 370 380

Ile Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln 385 390 395 400

Tyr Ser Met Leu Ala Thr Trp Arg Arg Thr Pro Arg Arg Glu Ala 405 410 415

Thr Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly
420 425 430

Cys Leu Glu Asp Ile Glu Glu Ala Leu Cys Gly Pro Ala Ala Leu Pro 435 440 445

Pro Ala Pro Ser Leu Leu Arg 450 455

<210> 28

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: N-terminal
 amino acid sequence of protein purified from urine
 (main sequence)

<220>

<221> UNSURE

<222> (4)

<223> identity of "Xaa" could not be determined

<400> 28

Asp Ser Val Xaa Pro Gln Gly Lys Tyr Ile His Pro Gln
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      (subsidiary sequence)
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ctacttgtac aatgactgtc caggcccggg gcaggatacg gactgcaggg agtgtgagag 120
cggctccttc acagcctcag aaaacaacaa g
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      cleavage peptide
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<222> (1)..(2)
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Asp Thr Val Cys Gly Cys Arg
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<223> identity of "Xaa" could not be determined
<220>
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<210> 40
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Thr Val Cys Gly
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<222> (6)
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cagggtaagt acatccatcc
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caaggcaaat atattcatcc	20
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## cleavage peptide

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Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Glu Asn Asn Lys
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Glu Cys Gly Ser Gly Ser Phe Thr Ala Ser Cys Asn Asn Lys
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	Provincian of Autificial Company, hybridization	
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aaatgt	ceggt cactettgtt gtteetaggg	30
_		
-2105	70 '	
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(443)		
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tcg cac aaa gga acc tac ttg tac aat gac tgt cca ggc ccg ggg cag Ser His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln 20 25 30	96
gat acg gac tgc agg gag tgt gag agc ggc tcc ttc aca gcc tca gaa Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu 35 40 45	144
aac aac aag gatcc	158

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Asn Asn Lys
     50
<210> 79
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Gln Gly Lys Tyr Ile His Pro Gln Asn Asn Ser Ile Ser Cys Thr Lys
Ser His Lys Gly Thr Tyr Leu Tyr Asn Asp Cys Pro Gly Pro Gly Gln
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Asp Thr Asp Cys Arg Glu Cys Glu Ser Gly Ser Phe Thr Ala Ser Glu
Asn Asn Lys
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oligonucleotide EBI-1820	
Oligonacieociae EBI-1820	
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-210. 01	
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universal primer	
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